SEQUENCE LISTING

<110> ITOH, Yasuaki
OGI, Kazuhiro
TANAKA, Hideyuki
KITADA, Chieko
<120> Novel Protein And Process For Producing Same
<130> 2543US0P
<150> PCT/JP99/04765
<151> 1999-09-02
<150> JP 10-250108
<151> 1998-09-03
<160> 19

<210> 1
<211> 119
<212> PRT
<213> Human
<400> 1

```
Met Lys Val Leu Ile Ser Ser Leu Leu Leu Leu Leu Pro Leu Met Leu
  1               5                  10                  15
Met Ser Met Val Ser Ser Ser Leu Asn Pro Gly Val Ala Arg Gly His
            20                  25                  30
Arg Asp Arg Gly Gln Ala Ser Arg Arg Trp Leu Gln Glu Gly Gly Gln
        35                  40                  45
Glu Cys Glu Cys Lys Asp Trp Phe Leu Arg Ala Pro Arg Arg Lys Phe
    50                  55                  60
Met Thr Val Ser Gly Leu Pro Lys Lys Gln Cys Pro Cys Asp His Phe
65                  70                  75                  80
Lys Gly Asn Val Lys Lys Thr Arg His Gln Arg His His Arg Lys Pro
                85                  90                  95
Asn Lys His Ser Arg Ala Cys Gln Gln Phe Leu Lys Gln Cys Gln Leu
            100                 105                 110
Arg Ser Phe Ala Leu Pro Leu
        115                 119
```

<210> 2
<211> 119
<212> PRT
<213> Rat
<400> 2

```
Met Lys Leu Leu Ala Ser Pro Phe Leu Leu Leu Leu Thr Gly Met Phe
  1               5                  10                  15
Thr Ala Thr Val Ser Ser Ser Pro Asn Gln Glu Val Ala Arg His His
            20                  25                  30
Gly Asp Gln His Gln Ala Pro Arg Arg Trp Leu Trp Glu Gly Gly Gln
        35                  40                  45
Glu Cys Asp Cys Lys Asp Trp Ser Leu Arg Val Ser Lys Arg Lys Thr
    50                  55                  60
Thr Ala Val Leu Glu Pro Pro Arg Lys Gln Cys Pro Cys Asp His Val
65                  70                  75                  80
Lys Gly Ser Glu Lys Lys Asn Arg Arg Gln Lys His His Arg Lys Ser
                85                  90                  95
Gln Arg Pro Ser Arg Thr Cys Gln Gln Phe Leu Lys Arg Cys Gln Leu
            100                 105                 110
Ala Ser Phe Ala Leu Pro Leu
        115                 119
```

<210> 3
<211> 119
<212> PRT
<213> Murine
<400> 3

```
Met Lys Leu Leu Ala Ser Pro Phe Leu Leu Leu Leu Pro Val Met Leu
  1               5                  10                  15
Met Ser Met Val Phe Ser Ser Pro Asn Pro Gly Val Ala Arg Ser His
            20                  25                  30
```

```
Gly Asp Gln His Leu Ala Pro Arg Arg Trp Leu Leu Glu Gly Gly Gln
          35                  40                  45
Glu Cys Glu Cys Lys Asp Trp Phe Leu Gln Ala Pro Lys Arg Lys Ala
      50                  55                  60
Thr Ala Val Leu Gly Pro Pro Arg Lys Gln Cys Pro Cys Asp His Val
 65                  70                  75                  80
Lys Gly Arg Glu Lys Lys Asn Arg His Gln Lys His His Arg Lys Ser
                 85                  90                  95
Gln Arg Pro Ser Arg Ala Cys Gln Gln Phe Leu Lys Arg Cys His Leu
            100                 105                 110
Ala Ser Phe Ala Leu Pro Leu
        115                 119
```

<210> 4
<211> 357
<212> DNA
<213> Human
<400> 4

```
ATGAAAGTTC TAATCTCTTC CCTCCTCCTG TTGCTGCCAC TAATGCTGAT GTCCATGGTC  60
TCTAGCAGCC TGAATCCAGG GGTCGCCAGA GGCCACAGGG ACCGAGGCCA GGCTTCTAGG 120
AGATGGCTCC AGGAAGGCGG CCAAGAATGT GAGTGCAAAG ATTGGTTCCT GAGAGCCCCG 180
AGAAGAAAAT TCATGACAGT GTCTGGGCTG CCAAAGAAGC AGTGCCCCTG TGATCATTTC 240
AAGGGCAATG TGAAGAAAAC AAGACACCAA AGGCACCACA GAAAGCCAAA CAAGCATTCC 300
AGAGCCTGCC AGCAATTTCT CAAACAATGT CAGCTAAGAA GCTTTGCTCT GCCTTTG    357
```

<210> 5
<211> 357
<212> DNA
<213> Rat
<400> 5

```
ATGAAGCTTC TAGCCTCTCC CTTCCTTCTG TTGCTGACAG GGATGTTCAC GGCCACGGTC  60
TCCAGCAGCC CGAATCAAGA GGTCGCCAGA CACCATGGGG ATCAACACCA GGCTCCTAGG 120
AGGTGGCTCT GGGAAGGTGG CCAAGAGTGT GACTGCAAAG ATTGGTCCCT GCGAGTCTCA 180
AAGAGAAAAA CCACAGCAGT GCTGGAGCCA CCAAGGAAGC AGTGTCCCTG TGATCATGTC 240
AAGGGCAGTG AGAAAAAGAA CAGACGCCAA AAGCACCACA GGAAGTCACA AAGGCCCTCC 300
AGAACCTGCC AGCAATTTCT CAAGCGATGT CAACTAGCAA GCTTCGCCCT GCCCTTA    357
```

<210> 6
<211> 357
<212> DNA
<213> Murine
<400> 6

```
ATGAAGCTTC TAGCCTCTCC CTTCCTTCTG TTGCTTCCAG TGATGCTCAT GTCCATGGTC  60
TTCAGCAGCC CGAACCCAGG GGTCGCCAGA AGCCACGGGG ACCAACACCT GGCTCCTAGG 120
AGGTGGCTCT TGGAAGGTGG CCAAGAATGT GAATGCAAAG ATTGGTTCCT GCAAGCCCCA 180
AAGAGAAAAG CCACAGCAGT GCTGGGGCCA CCAAGGAAGCA GTGTCCCTG TGATCACGTC 240
AAGGGCAGGG AGAAAAAAAA CAGACACCAA AAGCACCACA GGAAGTCGCA AAGACCCTCC 300
AGAGCCTGCC AGCAATTTCT CAAACGATGT CACCTGGCAA GCTTTGCGCT GCCCTTA    357
```

<210> 7
<211> 97
<212> PRT
<213> Artificial
<220>
<223> human fragment (23-119)
<400> 7

```
Ser Leu Asn Pro Gly Val Ala Arg Gly His Arg Asp Arg Gly Gln Ala
  1               5                  10                  15
Ser Arg Arg Trp Leu Gln Glu Gly Gly Gln Glu Cys Glu Cys Lys Asp
             20                  25                  30
Trp Phe Leu Arg Ala Pro Arg Arg Lys Phe Met Thr Val Ser Gly Leu
         35                  40                  45
Pro Lys Lys Gln Cys Pro Cys Asp His Phe Lys Gly Asn Val Lys Lys
     50                  55                  60
Thr Arg His Gln Arg His His Arg Lys Pro Asn Lys His Ser Arg Ala
 65                  70                  75                  80
Cys Gln Gln Phe Leu Lys Gln Cys Gln Leu Arg Ser Phe Ala Leu Pro
```

```
                85                  90                  95
Leu
 97

<210> 8
<211> 97
<212> PRT
<213> Artificial
<220>
<223> rat fragment (23-119)
<400> 8
Ser Pro Asn Gln Glu Val Ala Arg His His Gly Asp Gln His Gln Ala
  1               5                  10                  15
Pro Arg Arg Trp Leu Trp Glu Gly Gly Gln Glu Cys Asp Cys Lys Asp
            20                  25                  30
Trp Ser Leu Arg Val Ser Lys Arg Lys Thr Thr Ala Val Leu Glu Pro
        35                  40                  45
Pro Arg Lys Gln Cys Pro Cys Asp His Val Lys Gly Ser Glu Lys Lys
    50                  55                  60
Asn Arg Arg Gln Lys His His Arg Lys Ser Gln Arg Pro Ser Arg Thr
65                  70                  75                  80
Cys Gln Gln Phe Leu Lys Arg Cys Gln Leu Ala Ser Phe Ala Leu Pro
                85                  90                  95
Leu
 97

<210> 9
<211> 97
<212> PRT
<213> Artificial
<220>
<223> murine fragment (23-119)
<400> 9
Ser Pro Asn Pro Gly Val Ala Arg Ser His Gly Asp Gln His Leu Ala
  1               5                  10                  15
Pro Arg Arg Trp Leu Leu Glu Gly Gly Gln Glu Cys Glu Cys Lys Asp
            20                  25                  30
Trp Phe Leu Gln Ala Pro Lys Arg Lys Ala Thr Ala Val Leu Gly Pro
        35                  40                  45
Pro Arg Lys Gln Cys Pro Cys Asp His Val Lys Gly Arg Glu Lys Lys
    50                  55                  60

Asn Arg His Gln Lys His His Arg Lys Ser Gln Arg Pro Ser Arg Ala
65                  70                  75                  80
Cys Gln Gln Phe Leu Lys Arg Cys His Leu Ala Ser Phe Ala Leu Pro
                85                  90                  95
Leu
 97

<210> 10
<211> 291
<212> DNA
<213> Human
<400> 10
AGCCTGAATC CAGGGGTCGC CAGAGGCCAC AGGGACCGAG GCCAGGCTTC TAGGAGATGG  60
CTCCAGGAAG GCGGCCAAGA ATGTGAGTGC AAAGATTGGT TCCTGAGAGC CCCGAGAAGA 120
AAATTCATGA CAGTGTCTGG GCTGCCAAAG AAGCAGTGCC CCTGTGATCA TTTCAAGGGC 180
AATGTGAAGA AAACAAGACA CCAAAGGCAC CACAGAAAGC CAAACAAGCA TTCCAGAGCC 240
TGCCAGCAAT TTCTCAAACA ATGTCAGCTA AGAAGCTTTG CTCTGCCTTT G          291

<210> 11
<211> 291
<212> DNA
<213> Rat
<400> 11
AGCCCGAATC AAGAGGTCGC CAGACACCAT GGGGATCAAC ACCAGGCTCC TAGGAGGTGG  60
CTCTGGGAAG GTGGCCAAGA GTGTGACTGC AAAGATTGGT CCCTGCGAGT CTCAAAGAGA 120
```

AAAACCACAG CAGTGCTGGA GCCACCAAGG AAGCAGTGTC CCTGTGATCA TGTCAAGGGC 180
AGTGAGAAAA AGAACAGACG CCAAAAGCAC CACAGGAAGT CACAAAGGCC CTCCAGAACC 240
TGCCAGCAAT TTCTCAAGCG ATGTCAACTA GCAAGCTTCG CCCTGCCCTT A 291

<210> 12
<211> 291
<212> DNA
<213> Murine
<400> 12
AGCCCGAACC CAGGGGTCGC CAGAAGCCAC GGGGACCAAC ACCTGGCTCC TAGGAGGTGG 60
CTCTTGGAAG GTGGCCAAGA ATGTGAATGC AAAGATTGGT TCCTGCAAGC CCCAAAGAGA 120
AAAGCCACAG CAGTGCTGGG GCCACCAAGG AAGCAGTGTC CCTGTGATCA CGTCAAGGGC 180
AGGGAGAAAA AAAACAGACA CCAAAAGCAC CACAGGAAGT CGCAAAGACC CTCCAGAGCC 240
TGCCAGCAAT TTCTCAAACG ATGTCACCTG GCAAGCTTTG CGCTGCCCTT A 291

<210> 13
<211> 22
<212> DNA
<213> Artificial Sequence
<220>
<223> primer
<400> 13
GCCTTTAAGA ACCAACAGAC AG 22

<210> 14
<211> 40
<212> DNA
<213> Artificial Sequence
<220>
<223> primer
<400> 14
GACGAATTCC CACCATGAAA GTTCTAATCT CTTCCCTCCT 40

<210> 15
<211> 40
<212> DNA
<213> Artificial Sequence
<220>
<223> primer
<400> 15
GACTCGAGCG GCCGCTACAA AGGCAGAGCA AAGCTTCTTA 40

<210> 16
<211> 47
<212> DNA
<213> Artificial Sequence
<220>
<223> primer
<400> 16
TGCACCGTCG ACCACCATGA AAGTTCTAAT CTCTTCCCTC CTCCTGT 47

<210> 17
<211> 51
<212> DNA
<213> Artificial Sequence
<220>
<223> primer
<400> 17
CGCTCAGTCG ACCTACAAAG GCAGAGCAAA GCTTCTTAGC TGACATTGTT T 51

<210> 18
<211> 66
<212> DNA
<213> Artificial Sequence
<220>
<223> primer
<400> 18

ACAGCAGTCG ACCACCATGA AGCTTCTAGC CTCTCCCTTC CTTCTGTTGC TGACAGGGAT 60
GTTCAC 66

<210> 19
<211> 33
<212> DNA
<213> Artificial Sequence
<220>
<223> primer
<400> 19
CAGAGTGTCG ACACTATAAG GGCAGGGCGA AGC 33
1/8